

0280

# 3

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RAW SEQUENCE LISTING                      DATE: 02/09/2001  
 PATENT APPLICATION: US/09/771,956        TIME: 09:35:35

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3 <110> APPLICANT: Bennett, Michele  
 4     Brodbeck, Robbin  
 5     Krause, James  
 7 <120> TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 9 <130> FILE REFERENCE: N2000.001  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/771,956  
 C--> 12 <141> CURRENT FILING DATE: 2001-01-29  
 14 <160> NUMBER OF SEQ ID NOS: 31  
 16 <170> SOFTWARE: PatentIn Ver. 2.1  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 1605  
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 21 <213> ORGANISM: Homo sapiens  
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 25 ggaatgaaga attcagaata attttggttaa atggattcca atatggggaa taagaataag 120  
 26 ctgaacaggt gacctgcttt gaagaaacat actgtccatt tgtctaaaat aatctataac 180  
 27 aaccaaacca atcaaaatga attcaacatt atttccacag gttgaaaatc attcagttcca 240  
 28 ctctaatttc tcagagaaga atgccagctt tctggctttt gaaaatgatg attgtcatct 300  
 29 gcccttggcc atgatattta ccttagctct tgcctatgga gctgtgatac ttcttgggtg 360  
 30 ctctggaaac ctggccttga tcataatcat cttgaaacaa aaggagatga gaaatgttac 420  
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 34 tgtggaaacg catcagctga taatcaaccc tcgagggtgg agaccaaaata atagacatgc 660  
 35 ttatgtaggt attgtctgta ttgggtcctt tgcctgtggt tcttctttgc ctttctgat 720  
 36 ctaccaagta atgactgatg agccgttcca aaatgtaaca cttgatgcgt acaaagacaa 780  
 37 atacgtgtgc ttgatcaat ttccatcgga ctctcatagg ttgtcttata ccactctcct 840  
 38 cttggtgctg cagtattttt gtccactttg ttttatattt atttgctact tcaagatata 900  
 39 tatacgccca aaaaggagaa acaacatgat ggacaagatg agagacaata agtacaggtc 960  
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 42 ctgcaaccac aatctgttat tctgtctctg ccacctcaca gcaatgatat ccacttgtgt 1140  
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 55 <212> TYPE: PRT  
 56 <213> ORGANISM: Homo sapiens  
 58 <400> SEQUENCE: 2  
 59 Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His Ser

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60      1              5              10              15
62 Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn Asp Asp
63              20              25              30
65 Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly
66              35              40              45
68 Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile
69              50              55              60
71 Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val
72 65              70              75              80
74 Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe
75              85              90              95
77 Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met
78              100             105             110
80 Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile
81              115             120             125
83 Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn
84              130             135             140
86 Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala
87 145             150             155             160
89 Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr
90              165             170             175
92 Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr
93              180             185             190
95 Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg
96              195             200             205
98 Leu Ser Tyr Thr Thr Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu
99              210             215             220
101 Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
102 225             230             235             240
104 Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
105              245             250             255
107 Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe
108              260             265             270
110 Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp
111              275             280             285
113 Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu
114              290             295             300
116 Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
117 305             310             315             320
119 Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn
120              325             330             335
122 Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met
123              340             345             350
125 Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
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136 <211> LENGTH: 382

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/771,956  
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Input Set : A:\Npychimi1.app  
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145 20 25 30
147 His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu Ile Ile Ile Ile
148 35 40 45
150 Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile
151 50 55 60
153 Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn
154 65 70 75 80
156 Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr
157 85 90 95
159 Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys
160 100 105 110
162 Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe
163 115 120 125
165 Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro
166 130 135 140
168 Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val
169 145 150 155 160
171 Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln
172 165 170 175
174 Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys
175 180 185 190
177 Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu
178 195 200 205
180 Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
181 210 215 220
183 Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg
184 225 230 235 240
186 Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu
187 245 250 255
189 Thr Lys Arg Ile Asn Val Met Leu Leu Ser Ile Val Val Ala Phe Ala
190 260 265 270
192 Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn
193 275 280 285
195 His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys
196 290 295 300
198 His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly
199 305 310 315 320
201 Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe
202 325 330 335
204 Cys Asp Phe Arg Ser Arg Asp Asp Tyr Glu Thr Ile Ala Met Ser
205 340 345 350
207 Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro
208 355 360 365

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Input Set : A:\Npychiml.app  
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217 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 4
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221 cgacgagtat tataacaaga cacttgccac agagaataat actgctgcc ctcggaattc 120
222 tgatttccca gtctgggatg actataaaag cagtgtagat gacttacagt attttctgat 180
223 tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaatggc 240
224 tctcatgaaa aagcgtaatc agaagactac ggtaaacttc ctcataggca atctggcctt 300
225 ttctgataac ttggttgtgc tgttttgctc acctttcaca ctgacgtctg tcttgctgga 360
226 tcagtggaag ttggcgaag tcatgtgcc tttatgcct tttcttcaat gtgtgtcagt 420
227 tttggtttca actttaattt taatatcaat tgccattgct aggtatcata tgataaaaca 480
228 tcccatatct aataatttaa cagcaaacca tggctacttt ctgatagcta ctgtctggac 540
229 actaggtttt gccatctggt cctcccttcc agtgtttcac agtcttctgg aacttcaaga 600
230 aacatttggg tcagcattgc tgagcagcag gtatttatgt gttgagtcac ggccatctga 660
231 ttcatacaga attgctctta ctatctcttt attgctagt cagtatatcc tgcctctagt 720
232 ttgtcttact gtaagtata caagtgtctg cagaagtata agctgtggat tgtccaaaca 780
233 agaaaaacaga cttgaagaaa atgagatgat caacttaact ctctatccat ccaaaaaagag 840
234 tgggctctag gtgaaactct ctggcagcca taaatggagt tattcattca tcaaaaaaca 900
235 cagaagaaga tatagcaaga agacagcatg tgtgttacct gctccagaaa gacctctca 960
236 agagaaccac tccagaatac ttccagaaaa ctttggtctt gtaagaagtc agctctcttc 1020
237 atccagtaag ttcataccag ggtgccccac ttgctttgag ataaaaacct aagaaaattc 1080
238 agatgttcat gaattgagag taaaacgttc tgttacaaag ataaaaaaga gatctcgaag 1140
239 tgttttctac agactgacca tactgataat agtatttgct gttagtggga tgccactaca 1200
240 ccttttccat gtggttaactg attttaatga caatcttatt tcaaatagag atttcaagtt 1260
241 ggtgtattgc atttgtcatt tgttgggcag gatgtcctgt tgtcttaato caattctata 1320
242 tgggtttctt aataatggga ttaaagctga tttagtgtcc cttatacact gtcttcata 1380
243 gtaataatcc tcaactgtta ccaagg                      1406
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247 <211> LENGTH: 1069
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Description of Artificial Sequence:Y5/Y1 CHIMERA
254 <400> SEQUENCE: 5
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256 cgacgagtat tataacaaga cacttgccac agagaataat actgctgcc ctcggaattc 120
257 tgatttccca gtctgggatg actataaaag cagtgtagat gacttacagt attttctgat 180
258 tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaatggc 240
259 tctcatgaaa aagcgtaatc agaagactac ggtaaacttc ctcataggca atctggcctt 300
260 ttctgataac ttggttgtgc tgttttgctc acctttcaca ctgacgtctg tcttgctgga 360
261 tcagtggaag ttggcgaag tcatgtgcc tttatgcct tttcttcaat gtgtgtcagt 420
262 tttggtttca actttaattt taatatcaat tgccattgct aggtatcata tgataaaaca 480
263 tcccatatct aataatttaa cagcaaacca tggctacttt ctgatagcta ctgtctggac 540
264 actaggtttt gccatctggt cctcccttcc agtgtttcac agtcttctgg aacttcaaga 600
265 aacatttggg tcagcattgc tgagcagcag gtatttatgt gttgagtcac ggccatctga 660

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268 ggacaaagatg agagacaata agtacaggtc cagtagatct cgaagtgttt tctacagact 840
269 gaccatactg atattagtat ttgctgttag ttggatgccca ctacaccttt tccatgtggt 900
270 aactgatttt aatgacaatc ttatttcaaa taggcatttc aagttggtgt attgcatttg 960
271 tcatttggtg ggcattgatgt cctgttgtct taatccaatt ctatatgggt ttcttaataa 1020
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276 <211> LENGTH: 350
277 <212> TYPE: PRT
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
281 <223> OTHER INFORMATION: Description of Artificial Sequence:Y5/Y1 CHIMERA
283 <400> SEQUENCE: 6
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287 Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr
288 20 25 30
290 Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp
291 35 40 45
293 Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
294 50 55 60
296 Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
297 65 70 75 80
299 Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
300 85 90 95
302 Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
303 100 105 110
305 Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro
306 115 120 125
308 Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser
309 130 135 140
311 Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn
312 145 150 155 160
314 Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu
315 165 170 175
317 Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
318 180 185 190
320 Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys
321 195 200 205
323 Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser
324 210 215 220
326 Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser
327 225 230 235 240
329 His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met Asp
330 245 250 255
332 Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val Phe
333 260 265 270
335 Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro

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VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date